

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 10 | 510, 508
Source: PCT
Date Processed by STIC: 10 | 16 | 04

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PCT

RAW SEQUENCE LISTING

DATE: 10/16/2004

PATENT APPLICATION: US/10/510,508

TIME: 09:07:20

Input Set : A:\2543-1-038PCTUS - Seq List.txt

Output Set: N:\CRF4\10162004\J510508.raw

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3 <110> APPLICANT: Terrett, Jonathan A
5 <120> TITLE OF INVENTION: Protein Involved in Cancer
7 <130> FILE REFERENCE: 2543-1-038PCT/US
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/510,508
C--> 10 <141> CURRENT FILING DATE: 2004-10-07
12 <150> PRIOR APPLICATION NUMBER: GB0208332.7
13 <151> PRIOR FILING DATE: 2002-04-11
15 <150> PRIOR APPLICATION NUMBER: GB0229875.0
16 <151> PRIOR FILING DATE: 2002-12-21
18 <160> NUMBER OF SEQ ID NOS: 6
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1212
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
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33 20 25 30
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36 35 40 45
38 Ala Ser Arg Asp Gly Gly Gly Val Arg Asp Glu Gly Pro Ala Ala Ala
39 50 55 60
41 Gly Asp Gly Leu Gly Arg Pro Leu Gly Pro Thr Pro Ser Gln Ser Arg
42 65 70 75 80
44 Phe Gln Val Asp Leu Val Ser Glu Asn Ala Gly Arg Ala Ala Ala Ala
45 85 90 95
47 Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Ala Gly Ala Gly
48 100 105 110
50 Ala Lys Gln Thr Pro Ala Asp Gly Glu Ala Ser Gly Glu Ser Glu Pro
51 115 120 125
53 Ala Lys Gly Ser Glu Glu Ala Lys Gly Arg Phe Arg Val Asn Phe Val
54 130 135 140
56 Asp Pro Ala Ala Ser Ser Ser Ala Glu Asp Ser Leu Ser Asp Ala Ala
57 145 150 155 160
59 Gly Val Gly Val Asp Gly Pro Asn Val Ser Phe Gln Asn Gly Gly Asp
60 165 170 175
62 Thr Val Leu Ser Glu Gly Ser Ser Leu His Ser Gly Gly Gly Gly Gly
63 180 185 190
65 Ser Gly His His Gln His Tyr Tyr Tyr Asp Thr His Thr Asn Thr Tyr
66 195 200 205
68 Tyr Leu Arg Thr Phe Gly His Asn Thr Met Asp Ala Val Pro Arg Ile

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74 Pro Ser Leu Ala Glu Leu His Asp Glu Leu Glu Lys Glu Pro Phe Glu
75      245      250      255
77 Asp Gly Phe Ala Asn Gly Glu Glu Ser Thr Pro Thr Arg Asp Ala Val
78      260      265      270
80 Val Thr Tyr Thr Ala Glu Ser Lys Gly Val Val Lys Phe Gly Trp Ile
81      275      280      285
83 Lys Gly Val Leu Val Arg Cys Met Leu Asn Ile Trp Gly Val Met Leu
84      290      295      300
86 Phe Ile Arg Leu Ser Trp Ile Val Gly Gln Ala Gly Ile Gly Leu Ser
87 305      310      315      320
89 Val Leu Val Ile Met Met Ala Thr Val Val Thr Thr Ile Thr Gly Leu
90      325      330      335
92 Ser Thr Ser Ala Ile Ala Thr Asn Gly Phe Val Arg Gly Gly Gly Ala
93      340      345      350
95 Tyr Tyr Leu Ile Ser Arg Ser Leu Gly Pro Glu Phe Gly Gly Ala Ile
96      355      360      365
98 Gly Leu Ile Phe Ala Phe Ala Asn Ala Val Ala Val Ala Met Tyr Val
99      370      375      380
101 Val Gly Phe Ala Glu Thr Val Val Glu Leu Leu Lys Glu His Ser Ile
102 385      390      395      400
104 Leu Met Ile Asp Glu Ile Asn Asp Ile Arg Ile Ile Gly Ala Ile Thr
105      405      410      415
107 Val Val Ile Leu Leu Gly Ile Ser Val Ala Gly Met Glu Trp Glu Ala
108      420      425      430
110 Lys Ala Gln Ile Val Leu Leu Val Ile Leu Leu Leu Ala Ile Gly Asp
111      435      440      445
113 Phe Val Ile Gly Thr Phe Ile Pro Leu Glu Ser Lys Lys Pro Lys Gly
114      450      455      460
116 Phe Phe Gly Tyr Lys Ser Glu Ile Phe Asn Glu Asn Phe Gly Pro Asp
117 465      470      475      480
119 Phe Arg Glu Glu Glu Thr Phe Phe Ser Val Phe Ala Ile Phe Phe Pro
120      485      490      495
122 Ala Ala Thr Gly Ile Leu Ala Gly Ala Asn Ile Ser Gly Asp Leu Ala
123      500      505      510
125 Asp Pro Gln Ser Ala Ile Pro Lys Gly Thr Leu Leu Ala Ile Leu Ile
126      515      520      525
128 Thr Thr Leu Val Tyr Val Gly Ile Ala Val Ser Val Gly Ser Cys Val
129      530      535      540
131 Val Arg Asp Ala Thr Gly Asn Val Asn Asp Thr Ile Val Thr Glu Leu
132 545      550      555      560
134 Thr Asn Cys Thr Ser Ala Ala Cys Lys Leu Asn Phe Asp Phe Ser Ser
135      565      570      575
137 Cys Glu Ser Ser Pro Cys Ser Tyr Gly Leu Met Asn Asn Phe Gln Val
138      580      585      590
140 Met Ser Met Val Ser Gly Phe Thr Pro Leu Ile Ser Ala Gly Ile Phe
141      595      600      605

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147 625      630      635      640
149 Phe Ala Lys Gly Tyr Gly Lys Asn Asn Glu Pro Leu Arg Gly Tyr Ile
150      645      650      655
152 Leu Thr Phe Leu Ile Ala Leu Gly Phe Ile Leu Ile Ala Glu Leu Asn
153      660      665      670
155 Val Ile Ala Pro Ile Ile Ser Asn Phe Phe Leu Ala Ser Tyr Ala Leu
156      675      680      685
158 Ile Asn Phe Ser Val Phe His Ala Ser Leu Ala Lys Ser Pro Gly Trp
159      690      695      700
161 Arg Pro Ala Phe Lys Tyr Tyr Asn Met Trp Ile Ser Leu Leu Gly Ala
162 705      710      715      720
164 Ile Leu Cys Cys Ile Val Met Phe Val Ile Asn Trp Trp Ala Ala Leu
165      725      730      735
167 Leu Thr Tyr Val Ile Val Leu Gly Leu Tyr Ile Tyr Val Thr Tyr Lys
168      740      745      750
170 Lys Pro Asp Val Asn Trp Gly Ser Ser Thr Gln Ala Leu Thr Tyr Leu
171      755      760      765
173 Asn Ala Leu Gln His Ser Ile Arg Leu Ser Gly Val Glu Asp His Val
174      770      775      780
176 Lys Asn Phe Arg Pro Gln Cys Leu Val Met Thr Gly Ala Pro Asn Ser
177 785      790      795      800
179 Arg Pro Ala Leu Leu His Leu Val His Asp Phe Thr Lys Asn Val Gly
180      805      810      815
182 Leu Met Ile Cys Gly His Val His Met Gly Pro Arg Arg Gln Ala Met
183      820      825      830
185 Lys Glu Met Ser Ile Asp Gln Ala Lys Tyr Gln Arg Trp Leu Ile Lys
186      835      840      845
188 Asn Lys Met Lys Ala Phe Tyr Ala Pro Val His Ala Asp Asp Leu Arg
189      850      855      860
191 Glu Gly Ala Gln Tyr Leu Met Gln Ala Ala Gly Leu Gly Arg Met Lys
192 865      870      875      880
194 Pro Asn Thr Leu Val Leu Gly Phe Lys Lys Asp Trp Leu Gln Ala Asp
195      885      890      895
197 Met Arg Asp Val Asp Met Tyr Ile Asn Leu Phe His Asp Ala Phe Asp
198      900      905      910
200 Ile Gln Tyr Gly Val Val Val Ile Arg Leu Lys Glu Gly Leu Asp Ile
201      915      920      925
203 Ser His Leu Gln Gly Gln Glu Glu Leu Leu Ser Ser Gln Glu Lys Ser
204      930      935      940
206 Pro Gly Thr Lys Asp Val Val Val Ser Val Glu Tyr Ser Lys Lys Ser
207 945      950      955      960
209 Asp Leu Asp Thr Ser Lys Pro Leu Ser Glu Lys Pro Ile Thr His Lys
210      965      970      975
212 Val Glu Glu Glu Asp Gly Lys Thr Ala Thr Gln Pro Leu Leu Lys Lys
213      980      985      990
215 Glu Ser Lys Gly Pro Ile Val Pro Leu Asn Val Ala Asp Gln Lys Leu

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218 Leu Glu	Ala Ser Thr Gln Phe	Gln Lys Lys Gln Gly	Lys Asn Thr
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221 Ile Asp	Val Trp Trp Leu Phe	Asp Asp Gly Gly Leu	Thr Leu Leu
222 1025	1030	1035	
224 Ile Pro	Tyr Leu Leu Thr Thr	Lys Lys Lys Trp Lys	Asp Cys Lys
225 1040	1045	1050	
227 Ile Arg	Val Phe Ile Gly Gly	Lys Ile Asn Arg Ile	Asp His Asp
228 1055	1060	1065	
230 Arg Arg	Ala Met Ala Thr Leu	Leu Ser Lys Phe Arg	Ile Asp Phe
231 1070	1075	1080	
233 Ser Asp	Ile Met Val Leu Gly	Asp Ile Asn Thr Lys	Pro Lys Lys
234 1085	1090	1095	
236 Glu Asn	Ile Ile Ala Phe Glu	Glu Ile Ile Glu Pro	Tyr Arg Leu
237 1100	1105	1110	
239 His Glu	Asp Asp Lys Glu Gln	Asp Ile Ala Asp Lys	Met Lys Glu
240 1115	1120	1125	
242 Asp Glu	Pro Trp Arg Ile Thr	Asp Asn Glu Leu Glu	Leu Tyr Lys
243 1130	1135	1140	
245 Thr Lys	Thr Tyr Arg Gln Ile	Arg Leu Asn Glu Leu	Leu Lys Glu
246 1145	1150	1155	
248 His Ser	Ser Thr Ala Asn Ile	Ile Val Met Ser Leu	Pro Val Ala
249 1160	1165	1170	
251 Arg Lys	Gly Ala Val Ser Ser	Ala Leu Tyr Met Ala	Trp Leu Glu
252 1175	1180	1185	
254 Ala Leu	Ser Lys Asp Leu Pro	Pro Ile Leu Leu Val	Arg Gly Asn
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258 1205	1210		

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261 <211> LENGTH: 4098

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W--> 264 <400> SEQUENCE: 2

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269 agacgtccgc	cgggctctgc	agttccgcgc	ggggtcgggc	agctatggag	ccgcggccca	180
271 cggcgccttc	ctccggcgcc	ccgggactgg	ccggggtcgg	ggagacgccg	tcagccgctg	240
273 cgtggccgcg	agccaggggtg	gaactgcccg	gcacggctgt	gccctcggtg	ccggaggatg	300
275 ctgcccgcgc	gagccggggac	ggcggcgggg	tccgcgatga	gggccccgcg	gcggccgggg	360
277 acgggctggg	cagacccttg	gggcccaccc	cgagccagag	ccgtttccag	gtggacctgg	420
279 tttccgagaa	cgccgggctg	gcccgtgctg	cggcggcggc	ggcggcggcg	gcagcggcgg	480
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283 gcgagccagc	taaaggcagc	gaggaagcca	agggccgctt	ccgcgtgaac	ttcgtggacc	600
285 cagctgcctc	ctcgtcggtc	gaagacagcc	tgctcagatgc	tgccgggggtc	ggagtcgacg	660
287 ggcccaacgt	gagcttccag	aacggcgggg	acacgggtgt	gagcgagggc	agcagcctgc	720
289 actccggcgg	cggcggcggc	agtgggcacc	accagcacta	ctattatgat	acccacacca	780
291 acacctacta	cctgcgcacc	ttcggccaca	acaccatgga	cgctgtgccc	aggatcgatc	840
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389 ggtagaagc tctatctaag gacctaccac caatcctcct agttcgtggg aatcatcaga 3780
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